

AD05334;
 17-JUL-2001 (first entry)
 Human secreted protein-encoding gene 4 cDNA clone HMLFR02, SEQ ID NO:45.
 Human; secreted protein; proliferative disorder; cancer; tumour;
 foetal abnormality; developmental abnormality; haematopoietic disorder;
 immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 inflammation; allergy; neurological disorder; Alzheimer's disease;
 Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 cardiovascular disorder; angiogenic disorder; kidney disorder;
 gastrointestinal disorder; pregnancy-related disorder;
 endocrine disorder; infection; wound healing; vulvodynia;
 cell culture; chemotaxis; food additive; gene therapy;
 binding partner identification; chromosome 19; ss.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 166..1377
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 FT /product= "Human secreted protein"
 FT /transl_except= (pos:688..690, aa:Xaa)
 FT /transl_except= (pos:1123..1125, aa:Xaa)
 FT /transl_except= (pos:1156..1158, aa:Xaa)
 FT /transl_except= (pos:1267..1269, aa:Xaa)
 FT /note= "Xaa equals any of the twenty naturally occurring
 L-amino acids"
 FT sig_peptide 166..246
 FT /*tag= b
 FT mat_peptide 247..1374
 FT /*tag= c
 FT /product= "Mature human secreted protein"
 PN WO200134625-A1.
 XX 17-MAY-2001.
 XX 01-NOV-2000; 2000WO-US30045.
 XX 05-NOV-1999; 99US-0163581.
 XX 30-JUN-2000; 2000US-0215133.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Komatsoulis GA, Moore PA, Birse CE, Ni J;
 XX WPI; 2001-308778/32.
 XX P-PSDB; AA0501469.
 XX New nucleic acid molecules encoding 28 human secreted proteins for
 XX diagnosing, preventing, treating or ameliorating medical conditions and
 XX used as food additives or preservatives -
 PS Claim 1; Page 449; 562pp; English.
 XX AAD05300-AA05379 represent cDNAs corresponding to 28 human secreted
 CC protein genes, and AA051436-AA051513 represent the proteins they encode.
 CC AA051514-AA051544 represent human secreted protein fragments or variants.
 CC The genes and their secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 28 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,

skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
 CC cardiovascular disorders, angiogenic disorders, kidney disorders,
 CC gastrointestinal disorders, pregnancy-related disorders, endocrine
 CC disorders, and infections. The proteins can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues, to identify their
 CC cognate ligands or binding partners, and in chemotaxis, and can be used
 CC as a food additive or preservative to modify storage properties.
 CC Antibodies specific for a protein of the invention can be used in
 CC alleviating symptoms associated with the disorders mentioned above, and
 CC in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
 CC immunosorbent assay (ELISA). The present sequence represents a human
 CC secreted protein-encoding cDNA of the invention.
 XX Sequence 2086 BP: 544 A; 491 C; 538 G; 501 T; 12 other;
 SQ
 Query Match 84.3%; Score 1192.4; DB 22; Length 2086;
 Best Local Similarity 99.4%; Pred. No. 5.5e-283;
 Matches 1193; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 aggaaccccgaggaagggccgcgagatggcggtccctcaggggtcgtggcgagttcgcgg 60
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 QY 61 agcgtgggaagagcggaccctcgtctcccccgggtggtggccatggccacggcgagacg 120
 DB 123 agcgtgggaagagcggaccctcgtctcccccgggtggtggccatggccacggcgagacg 182
 QY 121 gagagccctcggcatcggctccagtggtctctcttggccactcgtggtctcatctgcgc 180
 DB 183 gagagccctcggcatcggctccagtggtctctcttggccactcgtggtctcatctgcgc 242
 QY 181 cgggcaagggggagcggagggatgggggtccagcctcgtcagcgggattggaactgta 240
 DB 243 cgggcaagggggagcggagggatgggggtccagcctcgtcagcgggattggaactgta 302
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 DB 303 cttcattttggacaaatcagggaagtgtcgtgcacactggaatggaatctattacttct 362
 QY 301 ggaacagttggttcacaaattcattcagccacagtcagtcagtccttcttcttcttc 360
 DB 363 ggaacagttggttcacaaattcattcagccacagtcagtcagtccttcttcttcttc 422
 QY 361 caccgaggaacaaaccttaataactgacagaagacagacagacaaatccgtcaaggcct 420
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 DB 483 agaagaactccagaaagtctccaggagagacacattacatgcatgagagattgaaag 542
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 DB 723 acagctggccggattgagcagatgaagatcgtgttctcccggtgaatgagcgtcttca 782
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OM nucleic - nucleic search, using sw model

Run on: August 8, 2002, 20:55:43 ; Search time 4666.15 Seconds
(without alignments)
6341.443 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
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- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
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- 27: em_sts.*
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- 29: em_vl.*
- 30: em_htg_hum.*
- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htg_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
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1	1414	100.0	1414	9	AF421380	Homo sapi
2	1193.8	84.4	5540	9	AF279145	Homo sapi
3	1052.4	74.4	2112	9	BC012074	Homo sapi
4	890	62.9	1436	9	AK001463	Mus muscu
5	853.4	60.4	5220	10	AF378762	Mus muscu
6	542.8	38.4	4007	9	AK025429	Homo sapi
7	255.8	18.1	2126	9	AK057316	Homo sapi
8	236	16.7	1297	9	BC012475	Homo sapi
9	232.2	16.4	2026	9	AK055636	Homo sapi
10	207.8	14.7	1343	9	AY040326	Homo sapi
11	194.4	13.7	8107	2	AC025010	Homo sapi
12	194.4	13.7	8107	2	AC025010	Homo sapi
13	113	8.0	1189	9	AK002160	Homo sapi
14	92.8	6.6	2557	10	BC003908	Mus muscu
15	62	4.4	16248	30	AC053530	Homo sapi
16	61.2	4.3	1512	10	BC010278	Mus muscu
17	61	4.3	8712	6	AX344694	Sequence
18	60.2	4.3	52359	2	AC010772	Homo sapi
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20	59.4	4.2	6070	6	AX281468	Sequence
21	59.4	4.2	6070	6	AX346581	Sequence
22	59.4	4.2	6070	6	AX348804	Sequence
23	59.4	4.2	6668	6	AX346598	Sequence
24	59.4	4.2	13712	6	AX346433	Sequence
25	59.2	4.2	9219	6	AX251565	Sequence
26	59.2	4.2	9219	6	AX347328	Sequence
27	59	4.2	349980	6	AX344558	Sequence
28	58.4	4.1	74412	2	AC020767	Homo sapi
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30	58	4.1	6283	6	AX345737	Sequence
31	58	4.1	6283	6	AX348379	Sequence
32	58	4.1	6944	6	AX347467	Sequence
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44	57	4.0	89128	2	AF001826	Homo sapi
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ALIGNMENTS

RESULT 1
AF421380

LOCUS AF421380 1414 bp mRNA linear PRI 13-NOV-2001
DEFINITION Homo sapiens anthrax toxin receptor mRNA, complete cds.

ACCESSION AF421380

VERSION AF421380.1 GI:16566412

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1414)

AUTHORS Bradley, K.A., Mogridge, J., Mourez, M., Collier, R.J. and Young, J.A.T.

TITLE Identification of the cellular receptor for anthrax toxin

JOURNAL Nature 414 (6860), 225-229 (2001)

MEDLINE 21557240

PUBMED 11700562

REMARK http://www.nature.com

REFERENCE 2 (bases 1 to 1414)

AUTHORS Bradley, K.A., Mogridge, J., Mourez, M., Collier, R.J. and Young, J.A.T.

TITLE Direct Submission

JOURNAL Submitted (19-SEP-2001) Department of Oncology, University of Wisconsin-Madison, 1400 University Ave., Madison, WI 53706, USA

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Qy	841	ccgacatgccgcaacgtggacagggtcctctcgagcttcaagaatcaatgactcgggtcac	900
Db	841	CCGACATGCCCGCAACGTGGACAGGGTCTCTGCAGCTTCAAGATCAATGACTCGGTTCAC	900
Qy	901	actcaatgagaagcccttttctgtggaagacacttatttactgtctcgagcgctatctt	960
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QY	661	acagctggcccgattgcggacagtaagatcatgtgttcccgtaagacagcgcttcca	720
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OM nucleic - nucleic search, using sw model

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(without alignments)
4951.169 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:

- 1: gb_da.*
- 2: gb_htg.*
- 3: gb_in.*
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- 5: gb_ov.*
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- 31: em_htg_inv.*
- 32: em_htg_other.*
- 33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	ID	Description
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1	1104	100.0	1414	9	AF421380	Homo sapi
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3	949.4	86.0	2112	9	BC012074	Homo sapi
4	853.4	77.3	5220	10	AF378762	Mus muscu
5	787	71.3	1436	9	AK001463	Homo sapi
6	542.8	49.2	4007	9	AK025429	Homo sapi
7	255.8	23.2	2126	9	AK057316	Homo sapi
8	236	21.4	1297	9	BC012475	Homo sapi
9	232.2	21.0	2026	9	AK055636	Homo sapi
10	207.8	18.8	1343	9	AY040326	Homo sapi
11	113	10.2	1189	9	AK002160	Homo sapi
12	92.8	8.4	2537	10	BC003908	Mus muscu
13	72.2	6.5	8107	2	AC025010	Homo sapi
14	48	4.3	1877	9	HS080080	Homo sapi
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17	44.4	4.0	229232	2	AC096624	Mus muscu
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25	40	3.6	158033	9	AC018926	Homo sapi
26	40	3.6	175264	9	AC011912	Homo sapi
27	40	3.6	235496	2	AC103312	Rattus no
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42	38	3.4	178295	2	AC021798	Homo sapi
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ALIGNMENTS

RESULT	1	AF421380	1414 bp	mrna	linear	PRI 13-NOV-2001
LOCUS		Homo sapiens anthrax toxin receptor mRNA, complete cds.				
DEFINITION		AF421380				
ACCESSION		AF421380.1				
VERSION		GI:16566412				
KEYWORDS		human.				
SOURCE		Homo sapiens				
ORGANISM		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE		1 (bases 1 to 1414)				
AUTHORS		Bradley, K.A., Mogridge, J., Mourez, M., Collier, R.J. and Young, J.A.T.				
TITLE		Identification of the cellular receptor for anthrax toxin				
JOURNAL		Nature 414 (6860), 225-229 (2001)				
MEDLINE		21557240				
PUBMED		11700562				
REMARK		http://www.nature.com				
REFERENCE		2 (bases 1 to 1414)				
AUTHORS		Bradley, K.A., Mogridge, J., Mourez, M., Collier, R.J. and Young, J.A.T.				
TITLE		Direct Submission				
JOURNAL		Submitted (19-SEP-2001) Department of Oncology, University of Wisconsin-Madison, 1400 University Ave., Madison, WI 53706, USA				

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REFERENCE 1 (bases 1 to 2112)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapps.rem@nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Suzanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guln,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smaluis, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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